(d) comparing the first-strand sequencing reads with the second-strand sequencing reads, and generating an error-corrected sequence of the double-stranded target nucleic acid molecule by distinguishing erroneous nucleotides in one strand that lack a matched base change in the complementary strand.

40. The method of claim 39, wherein the double-stranded target nucleic acid molecule comprises (i) a DNA molecule, or (ii) an RNA molecule.

41. The method of claim 39, wherein the cypher-target nucleic acid complex comprises at least two nucleic acid molecule priming sites.

42. The method of claim 39, wherein the cypher-target nucleic acid complex comprises an identifier sequence on both strands.

43. The method of claim 39, wherein the cypher-target nucleic acid complex comprises an identifier sequence at each end.

44. The method of claim 42, wherein the random or partially-random identifier sequence is double-stranded.

45. The method of claim 44, wherein the random or partially-random identifier sequence comprises about 5 to about 20 nucleotides.

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